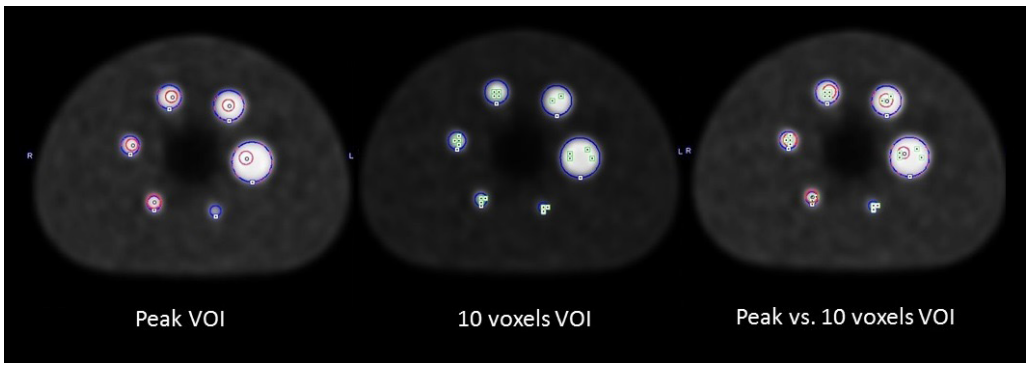

Figure S1 Comparison between peak and ten voxels VOIs in a transverse slice of the NEMA IEC Phantom. Blue contours represent the phantom spheres. In each sphere, the red circle represents the peak, and green voxels represent the ten hottest voxels. VOI, volume of interest.

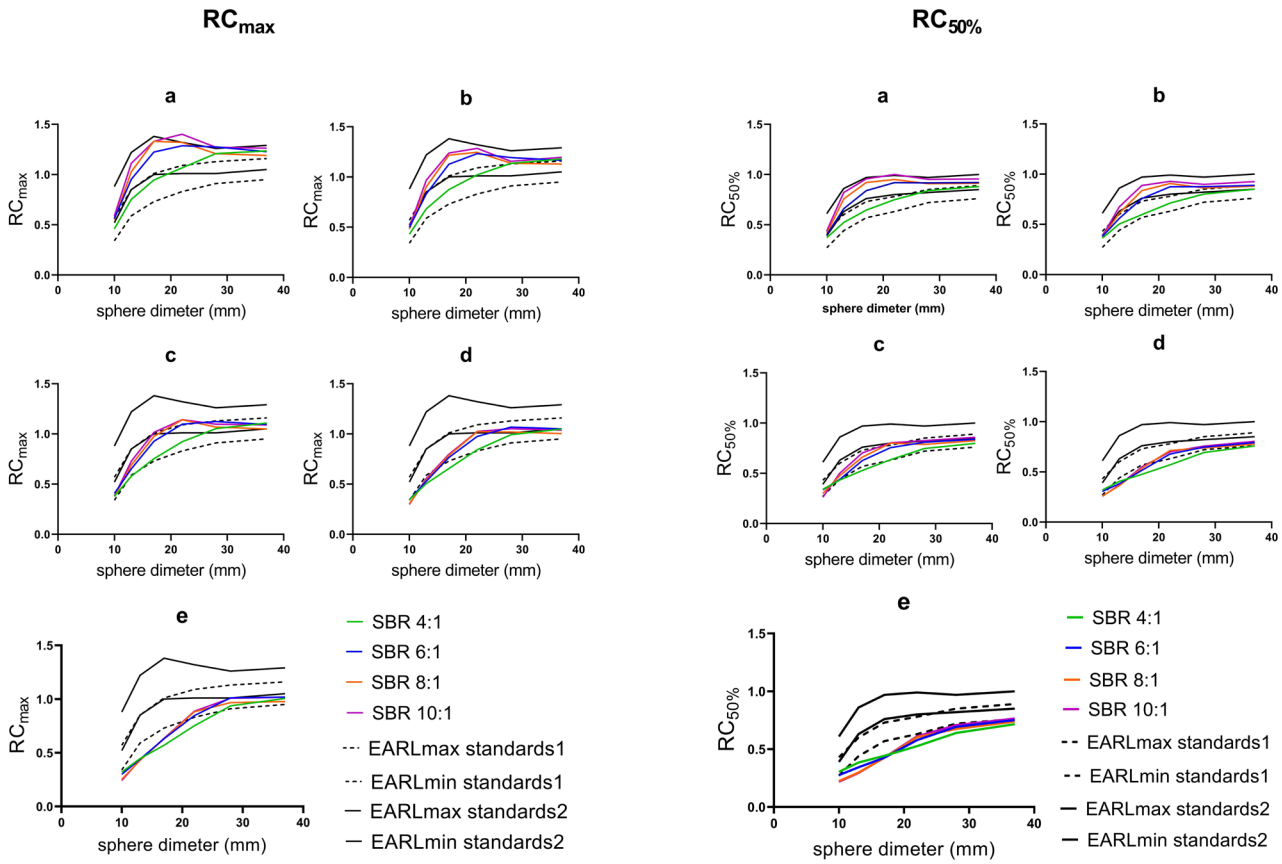

Figure S2 RC_{max} (left), and RC_{ISO-50} (right) curves against sphere sizes in reconstructed PET Images with sub-iterations 42 (PSF corrected) and various FWHM of Gaussian filter (a) 2 mm, (b) 4 mm, (c) 6 mm, (d) 8 mm and (e) 10 mm in Siemens Biograph6 TrueV PET/CT scanner. Although we observe nearly the same RC pattern in sphere diameters above 30 mm for all SBRs, low-contrasted spheres present a different behavior in the smaller spheres. PET/CT, positron emission tomography/computer tomography; RC, Recovery Coefficient; SBR, spheres-to-background ratios; FWHM, Full width at half maximum; PSF, point spread function.

https://dx.doi.org/10.21037/qims-22-443

Table S1 Statistical analysis using paired t-test between quantitative metrics derived from SBR10 and SBR4 reconstructed images

	Diameter of spheres					
	10 mm	13 mm	17 mm	22 mm	28 mm	37 mm
RC_{max}	0.25[#]	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
RC_{ISO-50}	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
RC_{peak}	–	0.80[#]	<0.0001	<0.0001	<0.0001	0.022

[#], P value >0.05 shows no statistically significant difference. (The statistical analysis of RC_{peak} for the smallest sphere is negligible because the volume size is less than 1 mL). SBR, spheres-to-background ratios; RC, recovery coefficient.

https://dx.doi.org/10.21037/qims-22-443

Table S2 The RMSE and curvature values for all RC metrics in both clinical and harmonized reconstruction settings in SBR4 and SBR10. A (set I) and B (set II) represent two different reconstruction sets in each scanner

	RC_{max}				RC_{ISO-50}				RC_{peak}							
	SBR 10		SBR 4		SBR 10		SBR 4		SBR 10		SBR 4		SBR 10		SBR 4	
	RMSE	Curvature	RMSE	Curvature	RMSE	Curvature	RMSE	Curvature	RMSE	Curvature	RMSE	Curvature	RMSE	Curvature	RMSE	Curvature
Standard clinical reconstruction setting																
Biograph mCT	0.28	0.28	0.30	0.35	0.31	0.24	0.30	0.25	0.34	0.38	0.32	0.38	0.30	0.36	0.29	0.38
Biograph6 TruePoint	0.22	0.24	0.30	0.41	0.32	0.20	0.40	0.27	0.36	0.34	0.37	0.38	0.27	0.31	0.33	0.39
Biograph6 TruePoint (TrueV)	0.27	0.28	0.28	0.39	0.27	0.22	0.38	0.27	0.34	0.37	0.35	0.36	0.27	0.31	0.29	0.39
Anyscan	0.46	0.54	0.41	0.51	0.55	0.38	0.54	0.32	0.53	0.51	0.50	0.39	0.47	0.54	0.42	0.48
Ingenuity TF-A	0.27	0.27	0.25	0.27	0.42	0.22	0.40	0.22	0.42	0.31	0.38	0.30	0.34	0.31	0.32	0.32
Ingenuity TF-B	0.25	0.27	0.26	0.28	0.30	0.20	0.31	0.22	0.32	0.30	0.33	0.32	0.28	0.32	0.28	0.34
Discovery 690-A	0.22	0.24	0.30	0.32	0.38	0.22	0.45	0.24	0.38	0.33	0.41	0.34	0.28	0.29	0.34	0.34
Discovery 690-B	0.18	0.20	0.27	0.26	0.35	0.20	0.42	0.22	0.36	0.32	0.40	0.32	0.24	0.26	0.30	0.29
Proposed harmonized reconstruction																
Biograph mCT-A	0.24	0.27	0.28	0.34	0.37	0.25	0.39	0.25	0.36	0.37	0.35	0.40	0.31	0.35	0.32	0.38
Biograph mCT-B	0.19	0.23	0.25	0.31	0.34	0.21	0.35	0.23	0.34	0.33	0.32	0.35	0.28	0.31	0.29	0.35
Biograph6 ruePoint (TrueV)-A	0.23	0.27	0.27	0.35	0.35	0.24	0.40	0.25	0.36	0.37	0.35	0.37	0.26	0.30	0.29	0.35
Biograph6 TruePoint (TrueV)-B	0.26	0.30	0.27	0.33	0.41	0.25	0.42	0.24	0.39	0.39	0.37	0.34	0.30	0.31	0.30	0.33
Biograph 6 TruePoint-A	0.23	0.24	0.29	0.36	0.39	0.22	0.42	0.24	0.38	0.34	0.38	0.36	0.30	0.30	0.33	0.35
Biograph 6 TruePoint-B	0.14	0.20	0.33	0.35	0.30	0.16	0.46	0.24	0.36	0.32	0.40	0.34	0.26	0.30	0.37	0.35
Ingenuity TF-A	0.25	0.27	0.28	0.30	0.37	0.22	0.41	0.25	0.36	0.32	0.38	0.32	0.32	0.32	0.33	0.35
Ingenuity TF-B	0.26	0.28	0.23	0.26	0.42	0.22	0.38	0.20	0.41	0.31	0.38	0.22	0.34	0.31	0.31	0.32
Discovery 690-A	0.22	0.24	0.30	0.32	0.38	0.22	0.45	0.24	0.38	0.33	0.41	0.34	0.28	0.29	0.34	0.34
Discovery 690-B	0.15	0.18	0.23	0.23	0.34	0.19	0.39	0.19	0.34	0.30	0.38	0.30	0.22	0.24	0.27	0.26

RMSE, root mean square error; RC, recovery coefficient; SBR, spheres-to-background ratio.

https://dx.doi.org/10.21037/qims-22-443